

# AlphaFold2 and its applications in the fields of biology and medicine

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## Abstract

AlphaFold2 (AF2) is an artificial intelligence (AI) system developed by DeepMind that can predict three-dimensional (3D) structures of proteins from amino acid sequences with atomic-level accuracy. Protein structure prediction is one of the most challenging problems in computational biology and chemistry, and has puzzled scientists for 50 years. The advent of AF2 presents an unprecedented progress in protein structure prediction and has attracted much attention. Subsequent release of structures of more than 200 million proteins predicted by AF2 further aroused great enthusiasm in the science community, especially in the fields of biology and medicine. AF2 is thought to have a significant impact on structural biology and research areas that need protein structure information, such as drug discovery, protein design, prediction of protein function, et al. Though the time is not long since AF2 was developed, there are already quite a few application studies of AF2 in the fields of biology and medicine, with many of them having preliminarily proved the potential of AF2. To better understand AF2 and promote its applications, we will in this article summarize the principle and system architecture of AF2 as well as the recipe of its success, and particularly focus on reviewing its applications in the fields of biology and medicine. Limitations of current AF2 prediction will also be discussed.